



GFI-108 sequence listing.ST25  
SEQUENCE LISTING

<110> GlycoFi, Inc.  
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Gerngross, Tilman U.  
Wildt, Stefan  
Choi, Byung-Kwon  
Nett, Juergen H.  
Davidson, Robert C.

<120> N-Acetylglucosaminyltransferase III expression in lower  
eukaryotes

<130> GFI-108 CIP

<140> US 10/680,963  
<141> 2003-10-07

<150> US 10/371,877  
<151> 2003-02-20

<150> US 09/892,591  
<151> 2001-06-27

<150> US 60/214,358  
<151> 2000-06-28

<150> US 60/215,638  
<151> 2000-06-30

<150> US 60/279,997  
<151> 2001-03-30

<150> PCT/US02/41510  
<151> 2002-12-24

<150> US 60/344,169  
<151> 2001-12-27

<160> 101

<170> PatentIn version 3.2

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<213> artificial

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<223> Primer A for target gene in P. pastoris (1,6-mannosyltransferase)

<400> 3

atggcgaagg cagatggcag t

21

<210> 4  
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 <212> DNA  
 <213> artificial

<220>  
 <223> Primer B for target gene in P. pastoris (1,6-mannosyltransferase)

<400> 4  
 ttagtccttc caacttcctt c

21

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 <212> DNA  
 <213> artificial

<220>  
 <223> Primer A for target gene in P. pastoris (1,2  
 mannosyltransferases)

<220>  
 <221> misc\_feature  
 <222> (9)..(9)  
 <223> wherein "n" is equal to "a" or "t" or "g" or "c".

<220>  
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 <223> wherein "n" is equal to "a" or "t" or "g" or "c".

<220>  
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 <223> wherein "n" is equal to "a" or "t" or "g" or "c".

<400> 5  
 taytggmgng tngarcynga yathaa

26

<210> 6  
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<220>  
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 mannosyltransferases)

<220>  
 <221> misc\_feature  
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<220>  
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 <222> (12)..(12)  
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GFI-108 sequence listing.ST25

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gcrtcncccc anckytcrta

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<210> 7  
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<210> 9  
<211> 458  
<212> PRT  
<213> *Saccharomyces cerevisiae*

<400> 9

Met Glu Gly Glu Gln Ser Pro Gln Gly Glu Lys Ser Leu Gln Arg Lys  
1 5 10 15

Gln Phe Val Arg Pro Pro Leu Asp Leu Trp Gln Asp Leu Lys Asp Gly  
20 25 30

Val Arg Tyr Val Ile Phe Asp Cys Arg Ala Asn Leu Ile Val Met Pro  
35 40 45

Leu Leu Ile Leu Phe Glu Ser Met Leu Cys Lys Ile Ile Ile Lys Lys  
50 55 60

Val Ala Tyr Thr Glu Ile Asp Tyr Lys Ala Tyr Met Glu Gln Ile Glu  
65 70 75 80

Met Ile Gln Leu Asp Gly Met Leu Asp Tyr Ser Gln Val Ser Gly Gly  
85 90 95

Thr Gly Pro Leu Val Tyr Pro Ala Gly His Val Leu Ile Tyr Lys Met  
100 105 110

Met Tyr Trp Leu Thr Glu Gly Met Asp His Val Glu Arg Gly Gln Val  
115 120 125

Phe Phe Arg Tyr Leu Tyr Leu Leu Thr Leu Ala Leu Gln Met Ala Cys  
130 135 140

Tyr Tyr Leu Leu His Leu Pro Pro Trp Cys Val Val Leu Ala Cys Leu  
145 150 155 160

Ser Lys Arg Leu His Ser Ile Tyr Val Leu Arg Leu Phe Asn Asp Cys  
Page 3

GFI-108 Sequence listing.ST25

165

170

175

Phe Thr Thr Leu Phe Met Val Val Thr Val Leu Gly Ala Ile Val Ala  
180 185 190

Ser Arg Cys His Gln Arg Pro Lys Leu Lys Lys Ser Leu Ala Leu Val  
195 200 205

Ile Ser Ala Thr Tyr Ser Met Ala Val Ser Ile Lys Met Asn Ala Leu  
210 215 220

Leu Tyr Phe Pro Ala Met Met Ile Ser Leu Phe Ile Leu Asn Asp Ala  
225 230 235 240

Asn Val Ile Leu Thr Leu Leu Asp Leu Val Ala Met Ile Ala Trp Gln  
245 250 255

Val Ala Val Ala Val Pro Phe Leu Arg Ser Phe Pro Gln Gln Tyr Leu  
260 265 270

His Cys Ala Phe Asn Phe Gly Arg Lys Phe Met Tyr Gln Trp Ser Ile  
275 280 285

Asn Trp Gln Met Met Asp Glu Glu Ala Phe Asn Asp Lys Arg Phe His  
290 295 300

Leu Ala Leu Leu Ile Ser His Leu Ile Ala Leu Thr Thr Leu Phe Val  
305 310 315 320

Thr Arg Tyr Pro Arg Ile Leu Pro Asp Leu Trp Ser Ser Leu Cys His  
325 330 335

Pro Leu Arg Lys Asn Ala Val Leu Asn Ala Asn Pro Ala Lys Thr Ile  
340 345 350

Pro Phe Val Leu Ile Ala Ser Asn Phe Ile Gly Val Leu Phe Ser Arg  
355 360 365

Ser Leu His Tyr Gln Phe Leu Ser Trp Tyr His Trp Thr Leu Pro Ile  
370 375 380

Leu Ile Phe Trp Ser Gly Met Pro Phe Phe Val Gly Pro Ile Trp Tyr  
385 390 395 400

Val Leu His Glu Trp Cys Trp Asn Ser Tyr Pro Pro Asn Ser Gln Ala  
405 410 415

GFI-108 Sequence listing.ST25

Ser Thr Leu Leu Leu Ala Leu Asn Thr Val Leu Leu Leu Leu Leu Ala  
420 425 430

Leu Thr Gln Leu Ser Gly Ser Val Ala Leu Ala Lys Ser His Leu Arg  
435 440 445

Thr Thr Ser Ser Met Glu Lys Lys Leu Asn  
450 455

<210> 10  
<211> 458  
<212> PRT  
<213> *Saccharomyces cerevisiae*

<400> 10

Met Glu Gly Glu Gln Ser Pro Gln Gly Glu Lys Ser Leu Gln Arg Lys  
1 5 10 15

Gln Phe Val Arg Pro Pro Leu Asp Leu Trp Gln Asp Leu Lys Asp Gly  
20 25 30

Val Arg Tyr Val Ile Phe Asp Cys Arg Ala Asn Leu Ile Val Met Pro  
35 40 45

Leu Leu Ile Leu Phe Glu Ser Met Leu Cys Lys Ile Ile Ile Lys Lys  
50 55 60

Val Ala Tyr Thr Glu Ile Asp Tyr Lys Ala Tyr Met Glu Gln Ile Glu  
65 70 75 80

Met Ile Gln Leu Asp Gly Met Leu Asp Tyr Ser Gln Val Ser Gly Gly  
85 90 95

Thr Gly Pro Leu Val Tyr Pro Ala Gly His Val Leu Ile Tyr Lys Met  
100 105 110

Met Tyr Trp Leu Thr Glu Gly Met Asp His Val Glu Arg Gly Gln Val  
115 120 125

Phe Phe Arg Tyr Leu Tyr Leu Leu Thr Leu Ala Leu Gln Met Ala Cys  
130 135 140

Tyr Tyr Leu Leu His Leu Pro Pro Trp Cys Val Val Leu Ala Cys Leu  
145 150 155 160

Ser Lys Arg Leu His Ser Ile Tyr Val Leu Arg Leu Phe Asn Asp Cys  
165 170 175

GFI-108 Sequence listing.ST25

Phe Thr Thr Leu Phe Met Val Val Thr Val Leu Gly Ala Ile Val Ala  
180 185 190

Ser Arg Cys His Gln Arg Pro Lys Leu Lys Lys Ser Leu Ala Leu Val  
195 200 205

Ile Ser Ala Thr Tyr Ser Met Ala Val Ser Ile Lys Met Asn Ala Leu  
210 215 220

Leu Tyr Phe Pro Ala Met Met Ile Ser Leu Phe Ile Leu Asn Asp Ala  
225 230 235 240

Asn Val Ile Leu Thr Leu Leu Asp Leu Val Ala Met Ile Ala Trp Gln  
245 250 255

Val Ala Val Ala Val Pro Phe Leu Arg Ser Phe Pro Gln Gln Tyr Leu  
260 265 270

His Cys Ala Phe Asn Phe Gly Arg Lys Phe Met Tyr Gln Trp Ser Ile  
275 280 285

Asn Trp Gln Met Met Asp Glu Glu Ala Phe Asn Asp Lys Arg Phe His  
290 295 300

Leu Ala Leu Leu Ile Ser His Leu Ile Ala Leu Thr Thr Leu Phe Val  
305 310 315 320

Thr Arg Tyr Pro Arg Ile Leu Pro Asp Leu Trp Ser Ser Leu Cys His  
325 330 335

Pro Leu Arg Lys Asn Ala Val Leu Asn Ala Asn Pro Ala Lys Thr Ile  
340 345 350

Pro Phe Val Leu Ile Ala Ser Asn Phe Ile Gly Val Leu Phe Ser Arg  
355 360 365

Ser Leu His Tyr Gln Phe Leu Ser Trp Tyr His Trp Thr Leu Pro Ile  
370 375 380

Leu Ile Phe Trp Ser Gly Met Pro Phe Phe Val Gly Pro Ile Trp Tyr  
385 390 395 400

Val Leu His Glu Trp Cys Trp Asn Ser Tyr Pro Pro Asn Ser Gln Ala  
405 410 415

Ser Thr Leu Leu Leu Ala Leu Asn Thr Val Leu Leu Leu Leu Leu Ala  
420 425 430

GFI-108 Sequence listing.ST25

Leu Thr Gln Leu Ser Gly Ser Val Ala Leu Ala Lys Ser His Leu Arg  
435 440 445

Thr Thr Ser Ser Met Glu Lys Lys Leu Asn  
450 455

<210> 11  
<211> 389  
<212> PRT  
<213> *Saccharomyces cerevisiae*

<400> 11

Trp Gln Asp Leu Lys Asp Gly Val Arg Tyr Val Ile Phe Asp Cys Arg  
1 5 10 15

Ala Asn Leu Ile Val Met Pro Leu Leu Ile Leu Phe Glu Ser Met Leu  
20 25 30

Cys Lys Ile Ile Ile Lys Lys Val Ala Tyr Thr Glu Ile Asp Tyr Lys  
35 40 45

Ala Tyr Met Glu Gln Ile Glu Met Ile Gln Leu Asp Gly Met Leu Asp  
50 55 60

Tyr Ser Gln Val Ser Gly Gly Thr Gly Pro Leu Val Tyr Pro Ala Gly  
65 70 75 80

His Val Leu Ile Tyr Lys Met Met Tyr Trp Leu Thr Glu Gly Met Asp  
85 90 95

His Val Glu Arg Gly Gln Val Phe Phe Arg Tyr Leu Tyr Leu Leu Thr  
100 105 110

Leu Ala Leu Gln Met Ala Cys Tyr Tyr Leu Leu His Leu Pro Pro Trp  
115 120 125

Cys Val Val Leu Ala Cys Leu Ser Lys Arg Leu His Ser Ile Tyr Val  
130 135 140

Leu Arg Leu Phe Asn Asp Cys Phe Thr Thr Leu Phe Met Val Val Thr  
145 150 155 160

Val Leu Gly Ala Ile Val Ala Ser Arg Cys His Gln Arg Pro Lys Leu  
165 170 175

Lys Lys Ser Leu Ala Leu Val Ile Ser Ala Thr Tyr Ser Met Ala Val  
180 185 190

GFI-108 Sequence listing.ST25

Ser Ile Lys Met Asn Ala Leu Leu Tyr Phe Pro Ala Met Met Ile Ser  
195 200 205

Leu Phe Ile Leu Asn Asp Ala Asn Val Ile Leu Thr Leu Leu Asp Leu  
210 215 220

Val Ala Met Ile Ala Trp Gln Val Ala Val Ala Val Pro Phe Leu Arg  
225 230 235 240

Ser Phe Pro Gln Gln Tyr Leu His Cys Ala Phe Asn Phe Gly Arg Lys  
245 250 255

Phe Met Tyr Gln Trp Ser Ile Asn Trp Gln Met Met Asp Glu Glu Ala  
260 265 270

Phe Asn Asp Lys Arg Phe His Leu Ala Leu Leu Ile Ser His Leu Ile  
275 280 285

Ala Leu Thr Thr Leu Phe Val Thr Arg Tyr Pro Arg Ile Leu Pro Asp  
290 295 300

Leu Trp Ser Ser Leu Cys His Pro Leu Arg Lys Asn Ala Val Leu Asn  
305 310 315 320

Ala Asn Pro Ala Lys Thr Ile Pro Phe Val Leu Ile Ala Ser Asn Phe  
325 330 335

Ile Gly Val Leu Phe Ser Arg Ser Leu His Tyr Gln Phe Leu Ser Trp  
340 345 350

Tyr His Trp Thr Leu Pro Ile Leu Ile Phe Trp Ser Gly Met Pro Phe  
355 360 365

Phe Val Gly Pro Ile Trp Tyr Val Leu His Glu Trp Cys Trp Asn Ser  
370 375 380

Tyr Pro Pro Asn Ser  
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<210> 12  
<211> 375  
<212> PRT  
<213> Homo sapiens

<400> 12

Trp Gln Glu Arg Arg Leu Leu Leu Arg Glu Pro Arg Tyr Thr Leu Leu  
1 5 10 15



GFI-108 Sequence listing.ST25

Val Ala Ala Cys<sub>20</sub> Leu Cys Leu Ala Glu<sub>25</sub> Val Gly Ile Thr Phe<sub>30</sub> Trp Val  
 Ile His Arg<sub>35</sub> Val Ala Tyr Thr Glu<sub>40</sub> Ile Asp Trp Lys<sub>45</sub> Ala Tyr Met Ala  
 Glu Val<sub>50</sub> Glu Gly Val Ile Asn<sub>55</sub> Gly Thr Tyr Asp Tyr<sub>60</sub> Thr Gln Leu Gln  
 Gly Asp Thr Gly Pro<sub>70</sub> Leu Val Tyr Pro Ala Gly<sub>75</sub> Phe Val Tyr Ile Phe<sub>80</sub>  
 Met Gly Leu Tyr Tyr<sub>85</sub> Ala Thr Ser Arg Gly<sub>90</sub> Thr Asp Ile Arg Met<sub>95</sub> Ala  
 Gln Asn Ile Phe<sub>100</sub> Ala Val Leu Tyr Leu<sub>105</sub> Ala Thr Leu Leu Leu<sub>110</sub> Val Phe  
 Leu Ile Tyr<sub>115</sub> His Gln Thr Cys Lys<sub>120</sub> Val Pro Pro Phe Val<sub>125</sub> Phe Phe Phe  
 Met Cys<sub>130</sub> Cys Ala Ser Tyr Arg<sub>135</sub> Val His Ser Ile Phe<sub>140</sub> Val Leu Arg Leu  
 Phe<sub>145</sub> Asn Asp Pro Val Ala<sub>150</sub> Met Val Leu Leu Phe<sub>155</sub> Leu Ser Ile Asn Leu<sub>160</sub>  
 Leu Leu Ala Gln Arg<sub>165</sub> Trp Gly Trp Gly Cys<sub>170</sub> Cys Phe Phe Ser Leu<sub>175</sub> Ala  
 Val Ser Val Lys<sub>180</sub> Met Asn Val Leu Leu<sub>185</sub> Phe Ala Pro Gly Leu<sub>190</sub> Leu Phe  
 Leu Leu Leu<sub>195</sub> Thr Gln Phe Gly Phe<sub>200</sub> Arg Gly Ala Leu Pro Lys Leu Gly  
 Ile Cys<sub>210</sub> Ala Gly Leu Gln Val<sub>215</sub> Val Leu Gly Leu Pro<sub>220</sub> Phe Leu Leu Glu  
 Asn<sub>225</sub> Pro Ser Gly Tyr Leu<sub>230</sub> Ser Arg Ser Phe Asp<sub>235</sub> Leu Gly Arg Gln Phe<sub>240</sub>  
 Leu Phe His Trp Thr<sub>245</sub> Val Asn Trp Arg Phe<sub>250</sub> Leu Pro Glu Ala Leu<sub>255</sub> Phe  
 Leu His Arg Ala<sub>260</sub> Phe His Leu Ala Leu<sub>265</sub> Leu Thr Ala His Leu<sub>270</sub> Thr Leu

GFI-108 Sequence listing.ST25

Leu Leu Leu Phe Ala Leu Cys Arg Trp His Arg Thr Gly Glu Ser Ile  
275 280 285

Leu Ser Leu Leu Arg Asp Pro Ser Lys Arg Lys Val Pro Pro Gln Pro  
290 295 300

Leu Thr Pro Asn Gln Ile Val Ser Thr Leu Phe Thr Ser Asn Phe Ile  
305 310 315 320

Gly Ile Cys Phe Ser Arg Ser Leu His Tyr Gln Phe Tyr Val Trp Tyr  
325 330 335

Phe His Thr Leu Pro Tyr Leu Leu Trp Ala Met Pro Ala Arg Trp Leu  
340 345 350

Thr His Leu Leu Arg Leu Leu Val Leu Gly Leu Ile Glu Leu Ser Trp  
355 360 365

Asn Thr Tyr Pro Ser Thr Ser  
370 375

<210> 13  
<211> 271  
<212> PRT  
<213> Saccharomyces cerevisiae  
<400> 13

Val Arg Tyr Val Ile Phe Asp Cys Arg Ala Asn Leu Ile Val Met Pro  
1 5 10 15

Leu Leu Ile Leu Phe Glu Ser Met Leu Cys Lys Ile Ile Ile Lys Lys  
20 25 30

Val Ala Tyr Thr Glu Ile Asp Tyr Lys Ala Tyr Met Glu Gln Ile Glu  
35 40 45

Met Ile Gln Leu Asp Gly Met Leu Asp Tyr Ser Gln Val Ser Gly Gly  
50 55 60

Thr Gly Pro Leu Val Tyr Pro Ala Gly His Val Leu Ile Tyr Lys Met  
65 70 75 80

Met Tyr Trp Leu Thr Glu Gly Met Asp His Val Glu Arg Gly Gln Val  
85 90 95

Phe Phe Arg Tyr Leu Tyr Leu Leu Thr Leu Ala Leu Gln Met Ala Cys  
100 105 110

GFI-108 Sequence listing.ST25

Tyr Tyr Leu Leu His Leu Pro Pro Trp Cys Val Val Leu Ala Cys Leu  
115 120 125

Ser Lys Arg Leu His Ser Ile Tyr Val Leu Arg Leu Phe Asn Asp Cys  
130 135 140

Phe Thr Thr Leu Phe Met Val Val Thr Val Leu Gly Ala Ile Val Ala  
145 150 155 160

Ser Arg Cys His Gln Arg Pro Lys Leu Lys Lys Ser Leu Ala Leu Val  
165 170 175

Ile Ser Ala Thr Tyr Ser Met Ala Val Ser Ile Lys Met Asn Ala Leu  
180 185 190

Leu Tyr Phe Pro Ala Met Met Ile Ser Leu Phe Ile Leu Asn Asp Ala  
195 200 205

Asn Val Ile Leu Thr Leu Leu Asp Leu Val Ala Met Ile Ala Trp Gln  
210 215 220

Val Ala Val Ala Val Pro Phe Leu Arg Ser Phe Pro Gln Gln Tyr Leu  
225 230 235 240

His Cys Ala Phe Asn Phe Gly Arg Lys Phe Met Tyr Gln Trp Ser Ile  
245 250 255

Asn Trp Gln Met Met Asp Glu Glu Ala Phe Asn Asp Lys Arg Phe  
260 265 270

<210> 14  
<211> 258  
<212> PRT  
<213> Drosophila virilis

<400> 14

Ile Lys Tyr Leu Ala Phe Glu Pro Ala Ala Leu Pro Ile Val Ser Val  
1 5 10 15

Leu Ile Val Leu Ala Glu Ala Val Ile Asn Val Leu Val Ile Gln Arg  
20 25 30

Val Pro Tyr Thr Glu Ile Asp Trp Lys Ala Tyr Met Gln Glu Cys Glu  
35 40 45

Gly Phe Leu Asn Gly Thr Thr Asn Tyr Ser Leu Leu Arg Gly Asp Thr  
50 55 60

GFI-108 Sequence listing.ST25

Gly Pro Leu Val Tyr Pro Ala Ala Phe Val Tyr Ile Tyr Ser Gly Leu  
65 70 75 80

Tyr Tyr Leu Thr Gly Gln Gly Thr Asn Val Arg Leu Ala Gln Tyr Ile  
85 90 95

Phe Ala Cys Ile Tyr Leu Leu Gln Met Cys Leu Val Leu Arg Leu Tyr  
100 105 110

Thr Lys Ser Arg Lys Val Pro Pro Tyr Val Leu Val Leu Ser Ala Phe  
115 120 125

Thr Ser Tyr Arg Ile His Ser Ile Tyr Val Leu Arg Leu Phe Asn Asp  
130 135 140

Pro Val Ala Ile Leu Leu Leu Tyr Ala Ala Leu Asn Leu Phe Leu Asp  
145 150 155 160

Gln Arg Trp Thr Leu Gly Ser Ile Cys Tyr Ser Leu Ala Val Gly Val  
165 170 175

Lys Met Asn Ile Leu Leu Phe Ala Pro Ala Leu Leu Leu Phe Tyr Leu  
180 185 190

Ala Asn Leu Gly Val Leu Arg Thr Leu Val Gln Leu Thr Ile Cys Ala  
195 200 205

Val Leu Gln Leu Phe Ile Gly Ala Pro Phe Leu Arg Thr His Pro Met  
210 215 220

Glu Tyr Leu Arg Gly Ser Phe Asp Leu Gly Arg Ile Phe Glu His Lys  
225 230 235 240

Trp Thr Val Asn Tyr Arg Phe Leu Ser Lys Glu Leu Phe Glu Gln Arg  
245 250 255

Glu Phe

<210> 15  
<211> 60  
<212> PRT  
<213> *Saccharomyces cerevisiae*  
  
<400> 15

Ile Pro Phe Val Leu Ile Ala Ser Asn Phe Ile Gly Val Leu Phe Ser  
1 5 10 15

GFI-108 Sequence listing.ST25

Arg Ser Leu His Tyr Gln Phe Leu Ser Trp Tyr His Trp Thr Leu Pro  
20 25 30

Ile Leu Ile Phe Trp Ser Gly Met Pro Phe Phe Val Gly Pro Ile Trp  
35 40 45

Tyr Val Leu His Glu Trp Cys Trp Asn Ser Tyr Pro  
50 55 60

<210> 16  
<211> 58  
<212> PRT  
<213> *Drosophila virilis*  
<400> 16

Leu Pro Phe Phe Leu Cys Asn Phe Ile Gly Val Ala Cys Ala Arg Ser  
1 5 10 15

Leu His Tyr Gln Phe Tyr Ile Trp Tyr Phe His Ser Leu Pro Tyr Leu  
20 25 30

Val Trp Ser Thr Pro Tyr Ser Leu Gly Val Arg Tyr Leu Ile Leu Gly  
35 40 45

Ile Ile Glu Tyr Cys Trp Asn Thr Tyr Pro  
50 55

<210> 17  
<211> 270  
<212> PRT  
<213> *Saccharomyces cerevisiae*  
<400> 17

Arg Tyr Val Ile Phe Asp Cys Arg Ala Asn Leu Ile Val Met Pro Leu  
1 5 10 15

Leu Ile Leu Phe Glu Ser Met Leu Cys Lys Ile Ile Ile Lys Lys Val  
20 25 30

Ala Tyr Thr Glu Ile Asp Tyr Lys Ala Tyr Met Glu Gln Ile Glu Met  
35 40 45

Ile Gln Leu Asp Gly Met Leu Asp Tyr Ser Gln Val Ser Gly Gly Thr  
50 55 60

Gly Pro Leu Val Tyr Pro Ala Gly His Val Leu Ile Tyr Lys Met Met  
65 70 75 80

GFI-108 Sequence listing.ST25

Tyr Trp Leu Thr Glu Gly Met Asp His Val Glu Arg Gly Gln Val Phe  
85 90 95

Phe Arg Tyr Leu Tyr Leu Leu Thr Leu Ala Leu Gln Met Ala Cys Tyr  
100 105 110

Tyr Leu Leu His Leu Pro Pro Trp Cys Val Val Leu Ala Cys Leu Ser  
115 120 125

Lys Arg Leu His Ser Ile Tyr Val Leu Arg Leu Phe Asn Asp Cys Phe  
130 135 140

Thr Thr Leu Phe Met Val Val Thr Val Leu Gly Ala Ile Val Ala Ser  
145 150 155 160

Arg Cys His Gln Arg Pro Lys Leu Lys Lys Ser Leu Ala Leu Val Ile  
165 170 175

Ser Ala Thr Tyr Ser Met Ala Val Ser Ile Lys Met Asn Ala Leu Leu  
180 185 190

Tyr Phe Pro Ala Met Met Ile Ser Leu Phe Ile Leu Asn Asp Ala Asn  
195 200 205

Val Ile Leu Thr Leu Leu Asp Leu Val Ala Met Ile Ala Trp Gln Val  
210 215 220

Ala Val Ala Val Pro Phe Leu Arg Ser Phe Pro Gln Gln Tyr Leu His  
225 230 235 240

Cys Ala Phe Asn Phe Gly Arg Lys Phe Met Tyr Gln Trp Ser Ile Asn  
245 250 255

Trp Gln Met Met Asp Glu Glu Ala Phe Asn Asp Lys Arg Phe  
260 265 270

<210> 18

<211> 257

<212> PRT

<213> Drosophila melanogaster

<400> 18

Lys Tyr Leu Leu Leu Glu Pro Ala Ala Leu Pro Ile Val Gly Leu Phe  
1 5 10 15

Val Leu Leu Ala Glu Leu Val Ile Asn Val Val Val Ile Gln Arg Val  
20 25 30

GFI-108 Sequence listing.ST25

Pro Tyr Thr Glu Ile Asp Trp Val Ala Tyr Met Gln Glu Cys Glu Gly  
35 40 45

Phe Leu Asn Gly Thr Thr Asn Tyr Ser Leu Leu Arg Gly Asp Thr Gly  
50 55 60

Pro Leu Val Tyr Pro Ala Ala Phe Val Tyr Ile Tyr Ser Ala Leu Tyr  
65 70 75 80

Tyr Val Thr Ser His Gly Thr Asn Val Arg Leu Ala Gln Tyr Ile Phe  
85 90 95

Ala Gly Ile Tyr Leu Leu Gln Leu Ala Leu Val Leu Arg Leu Tyr Ser  
100 105 110

Lys Ser Arg Lys Val Pro Pro Tyr Val Leu Val Leu Ser Ala Phe Thr  
115 120 125

Ser Tyr Arg Ile His Ser Ile Tyr Val Leu Arg Leu Phe Asn Asp Pro  
130 135 140

Val Ala Val Leu Leu Leu Tyr Ala Ala Leu Asn Leu Phe Leu Asp Arg  
145 150 155 160

Arg Trp Thr Leu Gly Ser Thr Phe Phe Ser Leu Ala Val Gly Val Lys  
165 170 175

Met Asn Ile Leu Leu Phe Ala Pro Ala Leu Leu Leu Phe Tyr Leu Ala  
180 185 190

Asn Leu Gly Leu Leu Arg Thr Ile Leu Gln Leu Ala Val Cys Gly Val  
195 200 205

Ile Gln Leu Leu Leu Gly Ala Pro Phe Leu Leu Thr His Pro Val Glu  
210 215 220

Tyr Leu Arg Gly Ser Phe Asp Leu Gly Arg Ile Phe Glu His Lys Trp  
225 230 235 240

Thr Val Asn Tyr Arg Phe Leu Ser Arg Asp Val Phe Glu Asn Arg Thr  
245 250 255

Phe

<210> 19  
<211> 60

GFI-108 Sequence listing.ST25

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 19

Ile Pro Phe Val Leu Ile Ala Ser Asn Phe Ile Gly Val Leu Phe Ser  
1 5 10 15

Arg Ser Leu His Tyr Gln Phe Leu Ser Trp Tyr His Trp Thr Leu Pro  
20 25 30

Ile Leu Ile Phe Trp Ser Gly Met Pro Phe Phe Val Gly Pro Ile Trp  
35 40 45

Tyr Val Leu His Glu Trp Cys Trp Asn Ser Tyr Pro  
50 55 60

<210> 20

<211> 58

<212> PRT

<213> *Drosophila melanogaster*

<400> 20

Leu Pro Phe Phe Leu Cys Asn Leu Val Gly Val Ala Cys Ser Arg Ser  
1 5 10 15

Leu His Tyr Gln Phe Tyr Val Trp Tyr Phe His Ser Leu Pro Tyr Leu  
20 25 30

Ala Trp Ser Thr Pro Tyr Ser Leu Gly Val Arg Cys Leu Ile Leu Gly  
35 40 45

Leu Ile Glu Tyr Cys Trp Asn Thr Tyr Pro  
50 55

<210> 21

<211> 1377

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 21

|  |     |
|--|-----|
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| cctccgctgg atctgtggca ggatctcaag gacggtgtgc gctacgtgat cttcgattgt  | 120 |
| aggccaatc ttatcgttat gccccttttg atttgttcg aaagcatgct gtgcaagatt    | 180 |
| atcattaaga aggtagctta cacagagatc gattacaagg cgtacatgga gcagatcgag  | 240 |
| atgattcagc tcgatggcat gctggactac tctcagggtga gtggtggaac gggcccgtg  | 300 |
| gtgtatccag caggccacgt cttgatctac aagatgatgt actggctaac agagggaatg  | 360 |
| gaccacgttg agcgcgggca agtgtttttc agatacttgt atctccttac actggcggtta | 420 |



GFI-108 Sequence listing.ST25

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caaatggcgt gttactacct ttacatcta ccaccgtggt gtgtggctctt ggcgtgcctc 480
tctaaaagat tgcactctat ttacgtgcta cggttattca atgattgctt cactactttg 540
tttatggtcg tcacggtttt gggggctatc gtggccagca ggtgccatca gcgccccaaa 600
ttaaagaagt cccttgcgct ggtgatctcc gcaacataca gtatggctgt gagcattaag 660
atgaatgcgc tgttgatatt ccctgcaatg atgatttctc tattcatcct taatgacgcg 720
aacgtaatcc ttactttggt ggatctcggt gcgatgattg catggcaagt cgcagttgca 780
gtgcccttcc tgcgcagctt tccgcaacag tacctgcatt gcgcttttaa tttcggcagg 840
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 <213> *Saccharomyces cerevisiae*

<400> 22

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Gln Phe Val Arg Pro Pro Leu Asp Leu Trp Gln Asp Leu Lys Asp Gly  
 20 25 30

Val Arg Tyr Val Ile Phe Asp Cys Arg Ala Asn Leu Ile Val Met Pro  
 35 40 45

Leu Leu Ile Leu Phe Glu Ser Met Leu Cys Lys Ile Ile Ile Lys Lys  
 50 55 60

Val Ala Tyr Thr Glu Ile Asp Tyr Lys Ala Tyr Met Glu Gln Ile Glu  
 65 70 75 80

Met Ile Gln Leu Asp Gly Met Leu Asp Tyr Ser Gln Val Ser Gly Gly  
 85 90 95

GFI-108 Sequence listing.ST25

Thr Gly Pro Leu Val Tyr Pro Ala Gly His Val Leu Ile Tyr Lys Met  
100 105 110

Met Tyr Trp Leu Thr Glu Gly Met Asp His Val Glu Arg Gly Gln Val  
115 120 125

Phe Phe Arg Tyr Leu Tyr Leu Leu Thr Leu Ala Leu Gln Met Ala Cys  
130 135 140

Tyr Tyr Leu Leu His Leu Pro Pro Trp Cys Val Val Leu Ala Cys Leu  
145 150 155 160

Ser Lys Arg Leu His Ser Ile Tyr Val Leu Arg Leu Phe Asn Asp Cys  
165 170 175

Phe Thr Thr Leu Phe Met Val Val Thr Val Leu Gly Ala Ile Val Ala  
180 185 190

Ser Arg Cys His Gln Arg Pro Lys Leu Lys Lys Ser Leu Ala Leu Val  
195 200 205

Ile Ser Ala Thr Tyr Ser Met Ala Val Ser Ile Lys Met Asn Ala Leu  
210 215 220

Leu Tyr Phe Pro Ala Met Met Ile Ser Leu Phe Ile Leu Asn Asp Ala  
225 230 235 240

Asn Val Ile Leu Thr Leu Leu Asp Leu Val Ala Met Ile Ala Trp Gln  
245 250 255

Val Ala Val Ala Val Pro Phe Leu Arg Ser Phe Pro Gln Gln Tyr Leu  
260 265 270

His Cys Ala Phe Asn Phe Gly Arg Lys Phe Met Tyr Gln Trp Ser Ile  
275 280 285

Asn Trp Gln Met Met Asp Glu Glu Ala Phe Asn Asp Lys Arg Phe His  
290 295 300

Leu Ala Leu Leu Ile Ser His Leu Ile Ala Leu Thr Thr Leu Phe Val  
305 310 315 320

Thr Arg Tyr Pro Arg Ile Leu Pro Asp Leu Trp Ser Ser Leu Cys His  
325 330 335

Pro Leu Arg Lys Asn Ala Val Leu Asn Ala Asn Pro Ala Lys Thr Ile

GFI-108 Sequence listing.ST25

340

345

350

Pro Phe Val Leu Ile Ala Ser Asn Phe Ile Gly Val Leu Phe Ser Arg  
355 360 365

Ser Leu His Tyr Gln Phe Leu Ser Trp Tyr His Trp Thr Leu Pro Ile  
370 375 380

Leu Ile Phe Trp Ser Gly Met Pro Phe Phe Val Gly Pro Ile Trp Tyr  
385 390 395 400

Val Leu His Glu Trp Cys Trp Asn Ser Tyr Pro Pro Asn Ser Gln Ala  
405 410 415

Ser Thr Leu Leu Leu Ala Leu Asn Thr Val Leu Leu Leu Leu Leu Ala  
420 425 430

Leu Thr Gln Leu Ser Gly Ser Val Ala Leu Ala Lys Ser His Leu Arg  
435 440 445

Thr Thr Ser Ser Met Glu Lys Lys Leu Asn  
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<210> 23

<211> 1395

<212> DNA

<213> Pichia pastoris

<400> 23

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|--|-----|
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| ctagtggctc ttattcaaaa cgttttatatt aaccagatt ttagtgtctt cgttgcacct  | 120 |
| cttttatggt tagctgattc cattgttatc aaggatgatca ttggcactgt ttcctacaca | 180 |
| gatattgatt tttcttcata tatgcaacaa atctttaaaa ttcgacaagg agaattagat  | 240 |
| tatagcaaca tttttggtga caccggtcca ttggtttacc cagccggcca tgttcatgct  | 300 |
| tactcagtac tttcgtggta cagtgatggt ggagaagacg tcagtttcgt tcaacaagca  | 360 |
| tttggttggt tatacctagg ttgcttggtta ctatccatca gtcctactt tttctctggc  | 420 |
| ttagggaaaa tacctccggt ttattttggt ttggttggtag cgtccaagag actgcattca | 480 |
| atatttgat tgagactctt caatgactgt ttaacaacat ttttgatggt ggcaactata   | 540 |
| atcatccttc aacaagcaag tagctggagg aaagatggca caactattcc attatctgtc  | 600 |
| cctgatgctg cagatacgta cagtttagcc atctctgtaa agatgaatgc gctgctatac  | 660 |
| ctcccagcat tcctactact catatatctc atttgtgacg aaaatttgat taaagccttg  | 720 |
| gcacctgttc tagttttgat attggtgcaa gtaggagtcg gttattcggt cattttaccg  | 780 |

GFI-108 Sequence listing.ST25

|   |      |
|---|------|
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| tttagtcgcc aatttcttta taagtggacg gttaattggc gctttttgag ccaagaaact   | 900  |
| ttcaacaatg tccattttca ccagctcctg tttgctctcc atattattac gttagtcttg   | 960  |
| ttcatcctca agttcctctc tcctaaaaac attggaaaac cgcttggtag atttgtgttg   | 1020 |
| gacattttca aattttggaa gccaacctta tctccaacca atattatcaa cgaccagaa    | 1080 |
| agaagccag attttggtta caccgtcatg gctactacca acttaatagg ggtgctttt     | 1140 |
| gcaagatctt tacactacca gttcctaagc tggatgcgt tctctttgcc atatctcctt    | 1200 |
| tacaaggctc gtctgaactt tatagcatct attattgttt atgccgctca cgagtattgc   | 1260 |
| tggttggttt tcccagctac agaacaaagt tccgcgttgt tggatctat cttactactt    | 1320 |
| atcctgattc tcatttttac caacgaacag ttatttcctt ctcaatcggc ccctgcagaa   | 1380 |
| aaaaagaata cataa  | 1395 |

<210> 24  
 <211> 464  
 <212> PRT  
 <213> Pichia pastoris

<400> 24

Met Pro Pro Ile Glu Pro Ala Glu Arg Pro Lys Leu Thr Leu Lys Asn  
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Val Ile Gly Asp Leu Val Ala Leu Ile Gln Asn Val Leu Phe Asn Pro  
 20 25 30

Asp Phe Ser Val Phe Val Ala Pro Leu Leu Trp Leu Ala Asp Ser Ile  
 35 40 45

Val Ile Lys Val Ile Ile Gly Thr Val Ser Tyr Thr Asp Ile Asp Phe  
 50 55 60

Ser Ser Tyr Met Gln Gln Ile Phe Lys Ile Arg Gln Gly Glu Leu Asp  
 65 70 75 80

Tyr Ser Asn Ile Phe Gly Asp Thr Gly Pro Leu Val Tyr Pro Ala Gly  
 85 90 95

His Val His Ala Tyr Ser Val Leu Ser Trp Tyr Ser Asp Gly Gly Glu  
 100 105 110

Asp Val Ser Phe Val Gln Gln Ala Phe Gly Trp Leu Tyr Leu Gly Cys  
 115 120 125

Leu Leu Leu Ser Ile Ser Ser Tyr Phe Phe Ser Gly Leu Gly Lys Ile  
 130 135 140

GFI-108 Sequence listing.ST25

130

135

140

Pro Pro Val Tyr Phe Val Leu Leu Val Ala Ser Lys Arg Leu His Ser  
145 150 155 160

Ile Phe Val Leu Arg Leu Phe Asn Asp Cys Leu Thr Thr Phe Leu Met  
165 170 175

Leu Ala Thr Ile Ile Ile Leu Gln Gln Ala Ser Ser Trp Arg Lys Asp  
180 185 190

Gly Thr Thr Ile Pro Leu Ser Val Pro Asp Ala Ala Asp Thr Tyr Ser  
195 200 205

Leu Ala Ile Ser Val Lys Met Asn Ala Leu Leu Tyr Leu Pro Ala Phe  
210 215 220

Leu Leu Leu Ile Tyr Leu Ile Cys Asp Glu Asn Leu Ile Lys Ala Leu  
225 230 235 240

Ala Pro Val Leu Val Leu Ile Leu Val Gln Val Gly Val Gly Tyr Ser  
245 250 255

Phe Ile Leu Pro Leu His Tyr Asp Asp Gln Ala Asn Glu Ile Arg Ser  
260 265 270

Ala Tyr Phe Arg Gln Ala Phe Asp Phe Ser Arg Gln Phe Leu Tyr Lys  
275 280 285

Trp Thr Val Asn Trp Arg Phe Leu Ser Gln Glu Thr Phe Asn Asn Val  
290 295 300

His Phe His Gln Leu Leu Phe Ala Leu His Ile Ile Thr Leu Val Leu  
305 310 315 320

Phe Ile Leu Lys Phe Leu Ser Pro Lys Asn Ile Gly Lys Pro Leu Gly  
325 330 335

Arg Phe Val Leu Asp Ile Phe Lys Phe Trp Lys Pro Thr Leu Ser Pro  
340 345 350

Thr Asn Ile Ile Asn Asp Pro Glu Arg Ser Pro Asp Phe Val Tyr Thr  
355 360 365

Val Met Ala Thr Thr Asn Leu Ile Gly Val Leu Phe Ala Arg Ser Leu  
370 375 380

GFI-108 Sequence listing.ST25

His Tyr Gln Phe Leu Ser Trp Tyr Ala Phe Ser Leu Pro Tyr Leu Leu  
385 390 395 400

Tyr Lys Ala Arg Leu Asn Phe Ile Ala Ser Ile Ile Val Tyr Ala Ala  
405 410 415

His Glu Tyr Cys Trp Leu Val Phe Pro Ala Thr Glu Gln Ser Ser Ala  
420 425 430

Leu Leu Val Ser Ile Leu Leu Leu Ile Leu Ile Leu Ile Phe Thr Asn  
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Glu Gln Leu Phe Pro Ser Gln Ser Val Pro Ala Glu Lys Lys Asn Thr  
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<210> 25  
<211> 423  
<212> PRT  
<213> Pichia pastoris

<400> 25

Arg Pro Lys Leu Thr Leu Lys Asn Val Ile Gly Asp Leu Val Ala Leu  
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Ile Gln Asn Val Leu Phe Asn Pro Asp Phe Ser Val Phe Val Ala Pro  
20 25 30

Leu Leu Trp Leu Ala Asp Ser Ile Val Ile Lys Val Ile Ile Gly Thr  
35 40 45

Val Ser Tyr Thr Asp Ile Asp Phe Ser Ser Tyr Met Gln Gln Ile Phe  
50 55 60

Lys Ile Arg Gln Gly Glu Leu Asp Tyr Ser Asn Ile Phe Gly Asp Thr  
65 70 75 80

Gly Pro Leu Val Tyr Pro Ala Gly His Val His Ala Tyr Ser Val Leu  
85 90 95

Ser Trp Tyr Ser Asp Gly Gly Glu Asp Val Ser Phe Val Gln Gln Ala  
100 105 110

Phe Gly Trp Leu Tyr Leu Gly Cys Leu Leu Leu Ser Ile Ser Ser Tyr  
115 120 125

Phe Phe Ser Gly Leu Gly Lys Ile Pro Pro Val Tyr Phe Val Leu Leu  
130 135 140

GFI-108 Sequence listing.ST25

Val Ala Ser Lys Arg Leu His Ser Ile Phe Val Leu Arg Leu Phe Asn  
145 150 155 160

Asp Cys Leu Thr Thr Phe Leu Met Leu Ala Thr Ile Ile Ile Leu Gln  
165 170 175

Gln Ala Ser Ser Trp Arg Lys Asp Gly Thr Thr Ile Pro Leu Ser Val  
180 185 190

Pro Asp Ala Ala Asp Thr Tyr Ser Leu Ala Ile Ser Val Lys Met Asn  
195 200 205

Ala Leu Leu Tyr Leu Pro Ala Phe Leu Leu Leu Ile Tyr Leu Ile Cys  
210 215 220

Asp Glu Asn Leu Ile Lys Ala Leu Ala Pro Val Leu Val Leu Ile Leu  
225 230 235 240

Val Gln Val Gly Val Gly Tyr Ser Phe Ile Leu Pro Leu His Tyr Asp  
245 250 255

Asp Gln Ala Asn Glu Ile Arg Ser Ala Tyr Phe Arg Gln Ala Phe Asp  
260 265 270

Phe Ser Arg Gln Phe Leu Tyr Lys Trp Thr Val Asn Trp Arg Phe Leu  
275 280 285

Ser Gln Glu Thr Phe Asn Asn Val His Phe His Gln Leu Leu Phe Ala  
290 295 300

Leu His Ile Ile Thr Leu Val Leu Phe Ile Leu Lys Phe Leu Ser Pro  
305 310 315 320

Lys Asn Ile Gly Lys Pro Leu Gly Arg Phe Val Leu Asp Ile Phe Lys  
325 330 335

Phe Trp Lys Pro Thr Leu Ser Pro Thr Asn Ile Ile Asn Asp Pro Glu  
340 345 350

Arg Ser Pro Asp Phe Val Tyr Thr Val Met Ala Thr Thr Asn Leu Ile  
355 360 365

Gly Val Leu Phe Ala Arg Ser Leu His Tyr Gln Phe Leu Ser Trp Tyr  
370 375 380

Ala Phe Ser Leu Pro Tyr Leu Leu Tyr Lys Ala Arg Leu Asn Phe Ile  
385 390 395 400

GFI-108 Sequence listing.ST25

Ala Ser Ile Ile Val Tyr Ala Ala His Glu Tyr Cys Trp Leu Val Phe  
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Pro Ala Thr Glu Gln Ser Ser  
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<210> 26

<211> 398

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 26

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Val Ile Phe Asp Cys Arg Ala Asn Leu Ile Val Met Pro Leu Leu Ile  
20 25 30

Leu Phe Glu Ser Met Leu Cys Lys Ile Ile Ile Lys Lys Val Ala Tyr  
35 40 45

Thr Glu Ile Asp Tyr Lys Ala Tyr Met Glu Gln Ile Glu Met Ile Gln  
50 55 60

Leu Asp Gly Met Leu Asp Tyr Ser Gln Val Ser Gly Gly Thr Gly Pro  
65 70 75 80

Leu Val Tyr Pro Ala Gly His Val Leu Ile Tyr Lys Met Met Tyr Trp  
85 90 95

Leu Thr Glu Gly Met Asp His Val Glu Arg Gly Gln Val Phe Phe Arg  
100 105 110

Tyr Leu Tyr Leu Leu Thr Leu Ala Leu Gln Met Ala Cys Tyr Tyr Leu  
115 120 125

Leu His Leu Pro Pro Trp Cys Val Val Leu Ala Cys Leu Ser Lys Arg  
130 135 140

Leu His Ser Ile Tyr Val Leu Arg Leu Phe Asn Asp Cys Phe Thr Thr  
145 150 155 160

Leu Phe Met Val Val Thr Val Leu Gly Ala Ile Val Ala Ser Arg Cys  
165 170 175

His Gln Arg Pro Lys Leu Lys Lys Ser Leu Ala Leu Val Ile Ser Ala  
180 185 190



GFI-108 Sequence listing.ST25

Thr Tyr Ser Met Ala Val Ser Ile Lys Met Asn Ala Leu Leu Tyr Phe  
195 200 205

Pro Ala Met Met Ile Ser Leu Phe Ile Leu Asn Asp Ala Asn Val Ile  
210 215 220

Leu Thr Leu Leu Asp Leu Val Ala Met Ile Ala Trp Gln Val Ala Val  
225 230 235 240

Ala Val Pro Phe Leu Arg Ser Phe Pro Gln Gln Tyr Leu His Cys Ala  
245 250 255

Phe Asn Phe Gly Arg Lys Phe Met Tyr Gln Trp Ser Ile Asn Trp Gln  
260 265 270

Met Met Asp Glu Glu Ala Phe Asn Asp Lys Arg Phe His Leu Ala Leu  
275 280 285

Leu Ile Ser His Leu Ile Ala Leu Thr Thr Leu Phe Val Thr Arg Tyr  
290 295 300

Pro Arg Ile Leu Pro Asp Leu Trp Ser Ser Leu Cys His Pro Leu Arg  
305 310 315 320

Lys Asn Ala Val Leu Asn Ala Asn Pro Ala Lys Thr Ile Pro Phe Val  
325 330 335

Leu Ile Ala Ser Asn Phe Ile Gly Val Leu Phe Ser Arg Ser Leu His  
340 345 350

Tyr Gln Phe Leu Ser Trp Tyr His Trp Thr Leu Pro Ile Leu Ile Phe  
355 360 365

Trp Ser Gly Met Pro Phe Phe Val Gly Pro Ile Trp Tyr Val Leu His  
370 375 380

Glu Trp Cys Trp Asn Ser Tyr Pro Pro Asn Ser Gln Ala Ser  
385 390 395

<210> 27  
<211> 398  
<212> PRT  
<213> Pichia pastoris

<400> 27

Ser Val Phe Val Ala Pro Leu Leu Trp Leu Ala Asp Ser Ile Val Ile  
1 5 10 15

GFI-108 Sequence listing.ST25

Lys Val Ile Ile Gly Thr Val Ser Tyr Thr Asp Ile Asp Phe Ser Ser  
20 25 30

Tyr Met Gln Gln Ile Phe Lys Ile Arg Gln Gly Glu Leu Asp Tyr Ser  
35 40 45

Asn Ile Phe Gly Asp Thr Gly Pro Leu Val Tyr Pro Ala Gly His Val  
50 55 60

His Ala Tyr Ser Val Leu Ser Trp Tyr Ser Asp Gly Gly Glu Asp Val  
65 70 75 80

Ser Phe Val Gln Gln Ala Phe Gly Trp Leu Tyr Leu Gly Cys Leu Leu  
85 90 95

Leu Ser Ile Ser Ser Tyr Phe Phe Ser Gly Leu Gly Lys Ile Pro Pro  
100 105 110

Val Tyr Phe Val Leu Leu Val Ala Ser Lys Arg Leu His Ser Ile Phe  
115 120 125

Val Leu Arg Leu Phe Asn Asp Cys Leu Thr Thr Phe Leu Met Leu Ala  
130 135 140

Thr Ile Ile Ile Leu Gln Gln Ala Ser Ser Trp Arg Lys Asp Gly Thr  
145 150 155 160

Thr Ile Pro Leu Ser Val Pro Asp Ala Ala Asp Thr Tyr Ser Leu Ala  
165 170 175

Ile Ser Val Lys Met Asn Ala Leu Leu Tyr Leu Pro Ala Phe Leu Leu  
180 185 190

Leu Ile Tyr Leu Ile Cys Asp Glu Asn Leu Ile Lys Ala Leu Ala Pro  
195 200 205

Val Leu Val Leu Ile Leu Val Gln Val Gly Val Gly Tyr Ser Phe Ile  
210 215 220

Leu Pro Leu His Tyr Asp Asp Gln Ala Asn Glu Ile Arg Ser Ala Tyr  
225 230 235 240

Phe Arg Gln Ala Phe Asp Phe Ser Arg Gln Phe Leu Tyr Lys Trp Thr  
245 250 255

Val Asn Trp Arg Phe Leu Ser Gln Glu Thr Phe Asn Asn Val His Phe  
260 265 270

GFI-108 Sequence listing.ST25

His Gln Leu Leu Phe Ala Leu His Ile Ile Thr Leu Val Leu Phe Ile  
275 280 285

Leu Lys Phe Leu Ser Pro Lys Asn Ile Gly Lys Pro Leu Gly Arg Phe  
290 295 300

Val Leu Asp Ile Phe Lys Phe Trp Lys Pro Thr Leu Ser Pro Thr Asn  
305 310 315 320

Ile Ile Asn Asp Pro Glu Arg Ser Pro Asp Phe Val Tyr Thr Val Met  
325 330 335

Ala Thr Thr Asn Leu Ile Gly Val Leu Phe Ala Arg Ser Leu His Tyr  
340 345 350

Gln Phe Leu Ser Trp Tyr Ala Phe Ser Leu Pro Tyr Leu Leu Tyr Lys  
355 360 365

Ala Arg Leu Asn Phe Ile Ala Ser Ile Ile Val Tyr Ala Ala His Glu  
370 375 380

Tyr Cys Trp Leu Val Phe Pro Ala Thr Glu Gln Ser Ser Ala  
385 390 395

<210> 28  
<211> 373  
<212> PRT  
<213> Neurospora crassa

<400> 28

Ser Lys Leu Ile Pro Pro Ala Leu Phe Leu Val Asp Ala Leu Leu Cys  
1 5 10 15

Gly Leu Ile Ile Trp Lys Val Pro Tyr Thr Glu Ile Asp Trp Ala Ala  
20 25 30

Tyr Met Glu Gln Val Ser Gln Ile Leu Ser Gly Glu Arg Asp Tyr Thr  
35 40 45

Lys Val Arg Gly Gly Thr Gly Pro Leu Val Tyr Pro Ala Ala His Val  
50 55 60

Tyr Ile Tyr Thr Gly Leu Tyr His Leu Thr Asp Glu Gly Arg Asn Ile  
65 70 75 80

Leu Leu Ala Gln Gln Leu Phe Ala Gly Leu Tyr Met Val Thr Leu Ala  
85 90 95

GFI-108 Sequence listing.ST25

Val Val Met Gly Cys Tyr Trp Gln Ala Lys Ala Pro Pro Tyr Leu Phe  
100 105 110

Pro Leu Leu Thr Leu Ser Lys Arg Leu His Ser Ile Phe Val Leu Arg  
115 120 125

Cys Phe Asn Asp Cys Phe Ala Val Leu Phe Leu Trp Leu Ala Ile Phe  
130 135 140

Phe Phe Gln Arg Arg Asn Trp Gln Ala Gly Ala Leu Leu Tyr Thr Leu  
145 150 155 160

Gly Leu Gly Val Lys Met Thr Leu Leu Leu Ser Leu Pro Ala Val Gly  
165 170 175

Ile Val Leu Phe Leu Gly Ser Gly Ser Phe Val Thr Thr Leu Gln Leu  
180 185 190

Val Ala Thr Met Gly Leu Val Gln Ile Leu Ile Gly Val Pro Phe Leu  
195 200 205

Ala His Tyr Pro Thr Glu Tyr Leu Ser Arg Ala Phe Glu Leu Ser Arg  
210 215 220

Gln Phe Phe Phe Lys Trp Thr Val Asn Trp Arg Phe Val Gly Glu Glu  
225 230 235 240

Ile Phe Leu Ser Lys Gly Phe Ala Leu Thr Leu Leu Ala Leu His Val  
245 250 255

Leu Val Leu Gly Ile Phe Ile Thr Thr Arg Trp Ile Lys Pro Ala Arg  
260 265 270

Lys Ser Leu Val Gln Leu Ile Ser Pro Val Leu Leu Ala Gly Lys Pro  
275 280 285

Pro Leu Thr Val Pro Glu His Arg Ala Ala Ala Arg Asp Val Thr Pro  
290 295 300

Arg Tyr Ile Met Thr Thr Ile Leu Ser Ala Asn Ala Val Gly Leu Leu  
305 310 315 320

Phe Ala Arg Ser Leu His Tyr Gln Phe Tyr Ala Tyr Val Ala Trp Ser  
325 330 335

Thr Pro Phe Leu Leu Trp Arg Ala Gly Leu His Pro Val Leu Val Tyr

GFI-108 Sequence listing.ST25

340

345

350

Leu Leu Trp Ala Val His Glu Trp Ala Trp Asn Val Phe Pro Ser Thr  
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Pro Ala Ser Ser Ala  
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<210> 29

<211> 390

<212> PRT

<213> Pichia pastoris

<400> 29

Leu Trp Leu Ala Asp Ser Ile Val Ile Lys Val Ile Ile Gly Thr Val  
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Ser Tyr Thr Asp Ile Asp Phe Ser Ser Tyr Met Gln Gln Ile Phe Lys  
20 25 30

Ile Arg Gln Gly Glu Leu Asp Tyr Ser Asn Ile Phe Gly Asp Thr Gly  
35 40 45

Pro Leu Val Tyr Pro Ala Gly His Val His Ala Tyr Ser Val Leu Ser  
50 55 60

Trp Tyr Ser Asp Gly Gly Glu Asp Val Ser Phe Val Gln Gln Ala Phe  
65 70 75 80

Gly Trp Leu Tyr Leu Gly Cys Leu Leu Leu Ser Ile Ser Ser Tyr Phe  
85 90 95

Phe Ser Gly Leu Gly Lys Ile Pro Pro Val Tyr Phe Val Leu Leu Val  
100 105 110

Ala Ser Lys Arg Leu His Ser Ile Phe Val Leu Arg Leu Phe Asn Asp  
115 120 125

Cys Leu Thr Thr Phe Leu Met Leu Ala Thr Ile Ile Ile Leu Gln Gln  
130 135 140

Ala Ser Ser Trp Arg Lys Asp Gly Thr Thr Ile Pro Leu Ser Val Pro  
145 150 155 160

Asp Ala Ala Asp Thr Tyr Ser Leu Ala Ile Ser Val Lys Met Asn Ala  
165 170 175

Leu Leu Tyr Leu Pro Ala Phe Leu Leu Leu Ile Tyr Leu Ile Cys Asp  
Page 29

GFI-108 sequence listing.ST25

180

185

190

Glu Asn Leu Ile Lys Ala Leu Ala Pro Val Leu Val Leu Ile Leu Val  
195 200 205

Gln Val Gly Val Gly Tyr Ser Phe Ile Leu Pro Leu His Tyr Asp Asp  
210 215 220

Gln Ala Asn Glu Ile Arg Ser Ala Tyr Phe Arg Gln Ala Phe Asp Phe  
225 230 235 240

Ser Arg Gln Phe Leu Tyr Lys Trp Thr Val Asn Trp Arg Phe Leu Ser  
245 250 255

Gln Glu Thr Phe Asn Asn Val His Phe His Gln Leu Leu Phe Ala Leu  
260 265 270

His Ile Ile Thr Leu Val Leu Phe Ile Leu Lys Phe Leu Ser Pro Lys  
275 280 285

Asn Ile Gly Lys Pro Leu Gly Arg Phe Val Leu Asp Ile Phe Lys Phe  
290 295 300

Trp Lys Pro Thr Leu Ser Pro Thr Asn Ile Ile Asn Asp Pro Glu Arg  
305 310 315 320

Ser Pro Asp Phe Val Tyr Thr Val Met Ala Thr Thr Asn Leu Ile Gly  
325 330 335

Val Leu Phe Ala Arg Ser Leu His Tyr Gln Phe Leu Ser Trp Tyr Ala  
340 345 350

Phe Ser Leu Pro Tyr Leu Leu Tyr Lys Ala Arg Leu Asn Phe Ile Ala  
355 360 365

Ser Ile Ile Val Tyr Ala Ala His Glu Tyr Cys Trp Leu Val Phe Pro  
370 375 380

Ala Thr Glu Gln Ser Ser  
385 390

<210> 30  
<211> 355  
<212> PRT  
<213> Schizosaccharomyces pombe

<400> 30

Leu Leu Leu Leu Glu Ile Pro Phe Val Phe Ala Ile Ile Ser Lys Val  
Page 30

GFI-108 Sequence listing.ST25

|             |                             |                     |                 |
|-------------|-----------------------------|---------------------|-----------------|
| 1           | 5                           | 10                  | 15              |
| Pro Tyr Thr | Glu Ile Asp Trp Ile         | Ala Tyr Met Glu Gln | Val Asn Ser     |
|             | 20                          | 25                  | 30              |
| Phe Leu Leu | Gly Glu Arg Asp Tyr         | Lys Ser Leu Val     | Gly Cys Thr Gly |
|             | 35                          | 40                  | 45              |
| Pro Leu Val | Tyr Pro Gly Gly His Val     | Phe Leu Tyr Thr     | Leu Leu Tyr     |
|             | 50                          | 55                  | 60              |
| Tyr Leu Thr | Asp Gly Gly Thr Asn Ile Val | Arg Ala Gln Tyr Ile | Phe             |
| 65          | 70                          | 75                  | 80              |
| Ala Phe Val | Tyr Trp Ile Thr Thr Ala     | Ile Val Gly Tyr Leu | Phe Lys         |
|             | 85                          | 90                  | 95              |
| Ile Val Arg | Ala Pro Phe Tyr Ile Tyr     | Val Leu Leu Ile     | Leu Ser Lys     |
|             | 100                         | 105                 | 110             |
| Arg Leu His | Ser Ile Phe Ile Leu Arg     | Leu Phe Asn Asp     | Gly Phe Asn     |
|             | 115                         | 120                 | 125             |
| Ser Leu Phe | Ser Ser Leu Phe Ile Leu     | Ser Ser Cys Lys     | Lys Lys Trp     |
|             | 130                         | 135                 | 140             |
| Val Arg Ala | Ser Ile Leu Leu Ser Val     | Ala Cys Ser Val     | Lys Met Ser     |
| 145         | 150                         | 155                 | 160             |
| Ser Leu Leu | Tyr Val Pro Ala Tyr Leu     | Val Leu Leu Leu     | Gln Ile Leu     |
|             | 165                         | 170                 | 175             |
| Gly Pro Lys | Lys Thr Trp Met His Ile     | Phe Val Ile Ile     | Ile Val Gln     |
|             | 180                         | 185                 | 190             |
| Ile Leu Phe | Ser Ile Pro Phe Leu Ala     | Tyr Phe Trp Ser     | Tyr Trp Thr     |
|             | 195                         | 200                 | 205             |
| Gln Ala Phe | Asp Phe Gly Arg Ala Phe     | Asp Tyr Lys Trp     | Thr Val Asn     |
|             | 210                         | 215                 | 220             |
| Trp Arg Phe | Ile Pro Arg Ser Ile Phe     | Glu Ser Thr Ser     | Phe Ser Thr     |
| 225         | 230                         | 235                 | 240             |
| Ser Ile Leu | Phe Leu His Val Ala Leu     | Leu Val Ala Phe     | Thr Cys Lys     |
|             | 245                         | 250                 | 255             |

GFI-108 Sequence listing.ST25

His Trp Asn Lys Leu Ser Arg Ala Thr Pro Phe Ala Met Val Asn Ser  
260 265 270

Met Leu Thr Leu Lys Pro Leu Pro Lys Leu Gln Leu Ala Thr Pro Asn  
275 280 285

Phe Ile Phe Thr Ala Leu Ala Thr Ser Asn Leu Ile Gly Ile Leu Cys  
290 295 300

Ala Arg Ser Leu His Tyr Gln Phe Tyr Ala Trp Phe Ala Trp Tyr Ser  
305 310 315 320

Pro Tyr Leu Cys Tyr Gln Ala Ser Phe Pro Ala Pro Ile Val Ile Gly  
325 330 335

Leu Trp Met Leu Gln Glu Tyr Ala Trp Asn Val Phe Pro Ser Thr Lys  
340 345 350

Leu Ser Ser  
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<210> 31  
<211> 390  
<212> PRT  
<213> Pichia pastoris

<400> 31

Leu Trp Leu Ala Asp Ser Ile Val Ile Lys Val Ile Ile Gly Thr Val  
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Ser Tyr Thr Asp Ile Asp Phe Ser Ser Tyr Met Gln Gln Ile Phe Lys  
20 25 30

Ile Arg Gln Gly Glu Leu Asp Tyr Ser Asn Ile Phe Gly Asp Thr Gly  
35 40 45

Pro Leu Val Tyr Pro Ala Gly His Val His Ala Tyr Ser Val Leu Ser  
50 55 60

Trp Tyr Ser Asp Gly Gly Glu Asp Val Ser Phe Val Gln Gln Ala Phe  
65 70 75 80

Gly Trp Leu Tyr Leu Gly Cys Leu Leu Leu Ser Ile Ser Ser Tyr Phe  
85 90 95

Phe Ser Gly Leu Gly Lys Ile Pro Pro Val Tyr Phe Val Leu Leu Val  
100 105 110



GFI-108 Sequence listing.ST25

Ala Ser Lys Arg Leu His Ser Ile Phe Val Leu Arg Leu Phe Asn Asp  
115 120 125

Cys Leu Thr Thr Phe Leu Met Leu Ala Thr Ile Ile Ile Leu Gln Gln  
130 135 140

Ala Ser Ser Trp Arg Lys Asp Gly Thr Thr Ile Pro Leu Ser Val Pro  
145 150 155 160

Asp Ala Ala Asp Thr Tyr Ser Leu Ala Ile Ser Val Lys Met Asn Ala  
165 170 175

Leu Leu Tyr Leu Pro Ala Phe Leu Leu Leu Ile Tyr Leu Ile Cys Asp  
180 185 190

Glu Asn Leu Ile Lys Ala Leu Ala Pro Val Leu Val Leu Ile Leu Val  
195 200 205

Gln Val Gly Val Gly Tyr Ser Phe Ile Leu Pro Leu His Tyr Asp Asp  
210 215 220

Gln Ala Asn Glu Ile Arg Ser Ala Tyr Phe Arg Gln Ala Phe Asp Phe  
225 230 235 240

Ser Arg Gln Phe Leu Tyr Lys Trp Thr Val Asn Trp Arg Phe Leu Ser  
245 250 255

Gln Glu Thr Phe Asn Asn Val His Phe His Gln Leu Leu Phe Ala Leu  
260 265 270

His Ile Ile Thr Leu Val Leu Phe Ile Leu Lys Phe Leu Ser Pro Lys  
275 280 285

Asn Ile Gly Lys Pro Leu Gly Arg Phe Val Leu Asp Ile Phe Lys Phe  
290 295 300

Trp Lys Pro Thr Leu Ser Pro Thr Asn Ile Ile Asn Asp Pro Glu Arg  
305 310 315 320

Ser Pro Asp Phe Val Tyr Thr Val Met Ala Thr Thr Asn Leu Ile Gly  
325 330 335

Val Leu Phe Ala Arg Ser Leu His Tyr Gln Phe Leu Ser Trp Tyr Ala  
340 345 350

Phe Ser Leu Pro Tyr Leu Leu Tyr Lys Ala Arg Leu Asn Phe Ile Ala  
355 360 365

GFI-108 Sequence listing.ST25

Ser Ile Ile Val Tyr Ala Ala His Glu Tyr Cys Trp Leu Val Phe Pro  
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Ala Thr Glu Gln Ser Ser  
385 390

<210> 32  
<211> 363  
<212> PRT  
<213> Arabidopsis thaliana

<400> 32

Leu Ile Leu Ala Asp Ala Ile Leu Val Ala Leu Ile Ile Ala Tyr Val  
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Pro Tyr Thr Lys Ile Asp Trp Asp Ala Tyr Met Ser Gln Val Ser Gly  
20 25 30

Phe Leu Gly Gly Glu Arg Asp Tyr Gly Asn Leu Lys Gly Asp Thr Gly  
35 40 45

Pro Leu Val Tyr Pro Ala Gly Phe Leu Tyr Val Tyr Ser Ala Val Gln  
50 55 60

Asn Leu Thr Gly Gly Glu Val Tyr Pro Ala Gln Ile Leu Phe Gly Val  
65 70 75 80

Leu Tyr Ile Val Asn Leu Gly Ile Val Leu Ile Ile Tyr Val Lys Thr  
85 90 95

Asp Val Val Pro Trp Trp Ala Leu Ser Leu Leu Cys Leu Ser Lys Arg  
100 105 110

Ile His Ser Ile Phe Val Leu Arg Leu Phe Asn Asp Cys Phe Ala Met  
115 120 125

Thr Leu Leu His Ala Ser Met Ala Leu Phe Leu Tyr Arg Lys Trp His  
130 135 140

Leu Gly Met Leu Val Phe Ser Gly Ala Val Ser Val Lys Met Asn Val  
145 150 155 160

Leu Leu Tyr Ala Pro Thr Leu Leu Leu Leu Leu Lys Ala Met Asn  
165 170 175

Ile Ile Gly Val Val Ser Ala Leu Ala Gly Ala Ala Leu Ala Gln Ile  
180 185 190

# GFI-108 Sequence listing.ST25

Leu Val Gly Leu Pro Phe Leu Ile Thr Tyr Pro Val Ser Tyr Ile Ala  
195 200 205

Asn Ala Phe Asp Leu Gly Arg Val Phe Ile His Phe Trp Ser Val Asn  
210 215 220

Phe Lys Phe Val Pro Glu Arg Val Phe Val Ser Lys Glu Phe Ala Val  
225 230 235 240

Cys Leu Leu Ile Ala His Leu Phe Leu Leu Val Ala Phe Ala Asn Tyr  
245 250 255

Lys Trp Cys Lys His Glu Gly Gly Ile Ile Gly Phe Met Arg Ser Arg  
260 265 270

His Phe Phe Leu Thr Leu Pro Ser Ser Leu Ser Phe Ser Asp Val Ser  
275 280 285

Ala Ser Arg Ile Ile Thr Lys Glu His Val Val Thr Ala Met Phe Val  
290 295 300

Gly Asn Phe Ile Gly Ile Val Phe Ala Arg Ser Leu His Tyr Gln Phe  
305 310 315 320

Tyr Ser Trp Tyr Phe Tyr Ser Leu Pro Tyr Leu Leu Trp Arg Thr Pro  
325 330 335

Phe Pro Thr Trp Leu Arg Leu Ile Met Phe Leu Gly Ile Glu Leu Cys  
340 345 350

Trp Asn Val Tyr Pro Ser Thr Pro Ser Ser Ser  
355 360

<210> 33  
<211> 428  
<212> DNA  
<213> Kluyveromyces lactis

<400> 33  
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gaacaaattg catacatttt acttgttacc aattacattg gagtactatt tgctcgatca 180  
ttacactacc aattcctatc ttggtacat tggacgttac cagtactatt gaattggggc 240  
aatgttccgt atccgctatg tgtgctatgg tacctaacac atgagtgggtg ctggaacagc 300  
tatccgcaa acgctactgc atccacactg ctacacgcgt gtaacacata ctgttattgg 360

## GFI-108 Sequence listing.ST25

ctgtattcctt aagaggaccc gcaaactcga aaagtgggtga taacgaaaca acacacgaga 420  
aagctgag 428

<210> 34  
<211> 142  
<212> PRT  
<213> Kluyveromyces lactis

<400> 34

Phe Val Tyr Lys Leu Ile Pro Thr Asn Met Asn Thr Pro Ala Gly Leu  
1 5 10 15

Leu Lys Ile Gly Lys Ala Asn Leu Leu His Pro Phe Thr Asp Ala Val  
20 25 30

Phe Ser Ala Met Arg Val Asn Ala Glu Gln Ile Ala Tyr Ile Leu Leu  
35 40 45

Val Thr Asn Tyr Ile Gly Val Leu Phe Ala Arg Ser Leu His Tyr Gln  
50 55 60

Phe Leu Ser Trp Tyr His Trp Thr Leu Pro Val Leu Leu Asn Trp Ala  
65 70 75 80

Asn Val Pro Tyr Pro Leu Cys Val Leu Trp Tyr Leu Thr His Glu Trp  
85 90 95

Cys Trp Asn Ser Tyr Pro Pro Asn Ala Thr Ala Ser Thr Leu Leu His  
100 105 110

Ala Cys Asn Thr Tyr Cys Tyr Trp Leu Tyr Ser Glx Glu Asp Pro Gln  
115 120 125

Thr Arg Lys Val Val Ile Thr Lys Gln His Thr Arg Lys Leu  
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<210> 35  
<211> 102  
<212> PRT  
<213> Kluyveromyces lactis

<400> 35

Ala Asn Leu Leu His Pro Phe Thr Asp Ala Val Phe Ser Ala Met Arg  
1 5 10 15

Val Asn Ala Glu Gln Ile Ala Tyr Ile Leu Leu Val Thr Asn Tyr Ile  
20 25 30

GFI-108 Sequence listing.ST25

Gly Val Leu Phe Ala Arg Ser Leu His Tyr Gln Phe Leu Ser Trp Tyr  
35 40 45

His Trp Thr Leu Pro Val Leu Leu Asn Trp Ala Asn Val Pro Tyr Pro  
50 55 60

Leu Cys Val Leu Trp Tyr Leu Thr His Glu Trp Cys Trp Asn Ser Tyr  
65 70 75 80

Pro Pro Asn Ala Thr Ala Ser Thr Leu Leu His Ala Cys Asn Thr Tyr  
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Cys Tyr Trp Leu Tyr Ser  
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<210> 36  
<211> 16  
<212> PRT  
<213> Kluyveromyces lactis

<400> 36

Glu Asp Pro Gln Thr Arg Lys Val Val Ile Thr Lys Gln His Thr Arg  
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<210> 37  
<211> 117  
<212> PRT  
<213> Saccharomyces cerevisiae

<400> 37

Ser Ser Leu Cys His Pro Leu Arg Lys Asn Ala Val Leu Asn Ala Asn  
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Pro Ala Lys Thr Ile Pro Phe Val Leu Ile Ala Ser Asn Phe Ile Gly  
20 25 30

Val Leu Phe Ser Arg Ser Leu His Tyr Gln Phe Leu Ser Trp Tyr His  
35 40 45

Trp Thr Leu Pro Ile Leu Ile Phe Trp Ser Gly Met Pro Phe Phe Val  
50 55 60

Gly Pro Ile Trp Tyr Val Leu His Glu Trp Cys Trp Asn Ser Tyr Pro  
65 70 75 80

Pro Asn Ser Gln Ala Ser Thr Leu Leu Leu Ala Leu Asn Thr Val Leu  
85 90 95

Leu Leu Leu Leu Ala Leu Thr Gln Leu Ser Gly Ser Val Ala Leu Ala  
Page 37

GFI-108 Sequence listing.ST25

100

105

110

Lys Ser His Leu Arg  
115

<210> 38  
<211> 96  
<212> PRT  
<213> Kluyveromyces lactis

<400> 38

Phe Thr Asp Ala Val Phe Ser Ala Met Arg Val Asn Ala Glu Gln Ile  
1 5 10 15

Ala Tyr Ile Leu Leu Val Thr Asn Tyr Ile Gly Val Leu Phe Ala Arg  
20 25 30

Ser Leu His Tyr Gln Phe Leu Ser Trp Tyr His Trp Thr Leu Pro Val  
35 40 45

Leu Leu Asn Trp Ala Asn Val Pro Tyr Pro Leu Cys Val Leu Trp Tyr  
50 55 60

Leu Thr His Glu Trp Cys Trp Asn Ser Tyr Pro Pro Asn Ala Thr Ala  
65 70 75 80

Ser Thr Leu Leu His Ala Cys Asn Thr Tyr Cys Tyr Trp Leu Tyr Ser  
85 90 95

<210> 39  
<211> 7  
<212> PRT  
<213> Kluyveromyces lactis

<400> 39

Glu Asp Pro Gln Thr Arg Lys  
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<210> 40  
<211> 106  
<212> PRT  
<213> Arabidopsis thaliana

<400> 40

Phe Ser Asp Val Ser Ala Ser Arg Ile Ile Thr Lys Glu His Val Val  
1 5 10 15

Thr Ala Met Phe Val Gly Asn Phe Ile Gly Ile Val Phe Ala Arg Ser  
20 25 30

GFI-108 Sequence listing.ST25

Leu His Tyr Gln Phe Tyr Ser Trp Tyr Phe Tyr Ser Leu Pro Tyr Leu  
35 40 45

Leu Trp Arg Thr Pro Phe Pro Thr Trp Leu Arg Leu Ile Met Phe Leu  
50 55 60

Gly Ile Glu Leu Cys Trp Asn Val Tyr Pro Ser Thr Pro Ser Ser Ser  
65 70 75 80

Gly Leu Leu Leu Cys Leu His Leu Ile Ile Leu Val Gly Leu Trp Leu  
85 90 95

Ala Pro Ser Val Asp Pro Tyr Gln Leu Lys  
100 105

<210> 41  
<211> 4  
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<213> artificial

<220>  
<223> signal tetrapeptide

<400> 41

His Asp Glu Leu  
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<210> 42  
<211> 4  
<212> PRT  
<213> artificial

<220>  
<223> signal tetrapeptide

<400> 42

Lys Asp Glu Leu  
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<210> 43  
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<210> 44  
<400> 44  
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<210> 45  
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<212> DNA  
<213> Mus musculus

## GFI-108 Sequence listing.ST25

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ctcagcccta acctcgatc cagcttcttc tggaacaatg cccctgtcac tccccaggcc    180
agtccggagc cgggtggccc cgacctattg cggacacccc tctactccca ctctcccctg    240
ctccagccac tgtccccgag caaggccaca gaggaactgc accgggtgga cttcgtgttg    300
ccggaggaca ccacggagta ttttgtgctc accaaagctg gtggtgtgtg cttcaaacca    360
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gatgcggacg agatccctgc gcgtgatggt gtgctgttcc taaaactcta cgatggctgg   1020
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ggcacactgg aggtggtgtc aggctgcacc atggacatgc tgcaggccgt gtatgggctg   1140
gatggcatcc gcctgcgccg ccgccagtac tacaccatgc ccaacttcg gcagtatgag   1200
aaccgcaccg gccacatcct agtgcagtgg tctctcggca gccccctgca cttcgcgggc   1260
tggcattgct cctggtgctt cacacccgag ggcattact ttaaactcgt gtcagcccag   1320
aatggcgact tccccgctg gggtgactat gaggacaaga gggacctcaa ttacatccgc   1380
agcttgatcc gactggggg atggttcgac ggaacgcagc aggagtacc tcctgcggac   1440
cccagtgagc acatgtatgc tcctaaatac ctgctcaaga actatgacca gttccgctac   1500
ttgctggaat atccctaccg ggagcccaag agcactgtag aggggtgggcg ccagaaccag   1560
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<210> 46
<211> 536
<212> PRT
<213> Mus musculus

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<400> 46

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GFI-108 Sequence listing.ST25

Met Arg Arg Tyr Lys Leu Phe Leu Met Phe Cys Met Ala Gly Leu Cys  
1 5 10 15

Leu Ile Ser Phe Leu His Phe Phe Lys Thr Leu Ser Tyr Val Thr Phe  
20 25 30

Pro Arg Glu Leu Ala Ser Leu Ser Pro Asn Leu Ile Ser Ser Phe Phe  
35 40 45

Trp Asn Asn Ala Pro Val Thr Pro Gln Ala Ser Pro Glu Pro Gly Asp  
50 55 60

Pro Asp Leu Leu Arg Thr Pro Leu Tyr Ser His Ser Pro Leu Leu Gln  
65 70 75 80

Pro Leu Ser Pro Ser Lys Ala Thr Glu Glu Leu His Arg Val Asp Phe  
85 90 95

Val Leu Pro Glu Asp Thr Thr Glu Tyr Phe Val Arg Thr Lys Ala Gly  
100 105 110

Gly Val Cys Phe Lys Pro Gly Thr Arg Met Leu Glu Lys Pro Ser Pro  
115 120 125

Gly Arg Thr Glu Glu Lys Thr Glu Val Ser Glu Gly Ser Ser Ala Arg  
130 135 140

Gly Pro Ala Arg Arg Pro Met Arg His Val Leu Ser Ser Arg Glu Arg  
145 150 155 160

Leu Gly Ser Arg Gly Thr Arg Arg Lys Trp Val Glu Cys Val Cys Leu  
165 170 175

Pro Gly Trp His Gly Pro Ser Cys Gly Val Pro Thr Val Val Gln Tyr  
180 185 190

Ser Asn Leu Pro Thr Lys Glu Arg Leu Val Pro Arg Glu Val Pro Arg  
195 200 205

Arg Val Ile Asn Ala Ile Asn Ile Asn His Glu Phe Asp Leu Leu Asp  
210 215 220

Val Arg Phe His Glu Leu Gly Asp Val Val Asp Ala Phe Val Val Cys  
225 230 235 240

Asp Ser Asn Phe Thr Ala Tyr Gly Glu Pro Arg Pro Leu Lys Phe Arg  
245 250 255

GFI-108 Sequence listing.ST25

Glu Met Leu Thr Asn Gly Thr Phe Glu Tyr Ile Arg His Lys Val Leu  
260 265 270

Tyr Val Phe Leu Asp His Phe Pro Pro Gly Gly Arg Gln Asp Gly Trp  
275 280 285

Ile Ala Asp Asp Tyr Leu Arg Thr Phe Leu Thr Gln Asp Gly Val Ser  
290 295 300

Arg Leu Arg Asn Leu Arg Pro Asp Asp Val Phe Ile Ile Asp Asp Ala  
305 310 315 320

Asp Glu Ile Pro Ala Arg Asp Gly Val Leu Phe Leu Lys Leu Tyr Asp  
325 330 335

Gly Trp Thr Glu Pro Phe Ala Phe His Met Arg Lys Ser Leu Tyr Gly  
340 345 350

Phe Phe Trp Lys Gln Pro Gly Thr Leu Glu Val Val Ser Gly Cys Thr  
355 360 365

Met Asp Met Leu Gln Ala Val Tyr Gly Leu Asp Gly Ile Arg Leu Arg  
370 375 380

Arg Arg Gln Tyr Tyr Thr Met Pro Asn Phe Arg Gln Tyr Glu Asn Arg  
385 390 395 400

Thr Gly His Ile Leu Val Gln Trp Ser Leu Gly Ser Pro Leu His Phe  
405 410 415

Ala Gly Trp His Cys Ser Trp Cys Phe Thr Pro Glu Gly Ile Tyr Phe  
420 425 430

Lys Leu Val Ser Ala Gln Asn Gly Asp Phe Pro Arg Trp Gly Asp Tyr  
435 440 445

Glu Asp Lys Arg Asp Leu Asn Tyr Ile Arg Ser Leu Ile Arg Thr Gly  
450 455 460

Gly Trp Phe Asp Gly Thr Gln Gln Glu Tyr Pro Pro Ala Asp Pro Ser  
465 470 475 480

Glu His Met Tyr Ala Pro Lys Tyr Leu Leu Lys Asn Tyr Asp Gln Phe  
485 490 495

Arg Tyr Leu Leu Glu Asn Pro Tyr Arg Glu Pro Lys Ser Thr Val Glu

GFI-108 Sequence listing.ST25

500

505

510

Gly Gly Arg Gln Asn Gln Gly Ser Asp Gly Arg Ser Ser Ala Val Arg  
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Gly Lys Leu Asp Thr Ala Glu Gly  
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<210> 47  
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<212> DNA  
<213> artificial

<220>  
<223> cloning primer

<400> 47  
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<210> 48  
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<213> artificial

<220>  
<223> cloning primer

<400> 48  
gtaatacgac tcactatagg gc 22

<210> 49  
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<212> DNA  
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<220>  
<223> cloning primer

<400> 49  
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<210> 50  
<211> 1968  
<212> DNA  
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<400> 50  
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accgagaagt tcgtgctgct gctggtgttc agcgccttca tcacgctctg cttcggggca 180  
atcttcttcc tgctgactc ctccaagctg ctacgcgggg tcctgttcca ctccaaccct 240  
gccttgacgc cgccggcgga gcacaagccc gggctcgggg cgcgtgcgga ggatgccgcc 300

GFI-108 Sequence listing.ST25

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|--|------|
| gaggggagag tccggcaccg cgaggaaggc gcgcttgggg accctggagc tggactggaa  | 360  |
| gacaacttag ccaggatccg cgaaaaccac gagcgggctc tcaggggaagc caaggagacc | 420  |
| ctgcagaagc tgccggagga gatccaaaga gacattctgc tggagaagga aaaggtggcc  | 480  |
| caggaccagc tgcgtgacaa ggatctgttt aggggcttgc ccaaggtgga cttcctgccc  | 540  |
| cccgtcgggg tagagaaccg ggagcccgtc gacgccacca tccgtgagaa gagggcaaag  | 600  |
| atcaaagaga tgatgacca tgcttggaa aattataaac gctatgcgtg gggcttgaac    | 660  |
| gaactgaaac ctatatcaaa agaaggccat tcaagcagtt tgtttgcaa catcaaagga   | 720  |
| gctacaatag tagatgccct ggataccctt ttcattatgg gcatgaagac tgaatttcaa  | 780  |
| gaagctaaat cgtggattaa aaaatattta gattttaatg tgaatgctga agtttctgtt  | 840  |
| tttgaagtca acatacgctt cgtcggtgga ctgctgtcag cctactattt gtccggagag  | 900  |
| gagatatttc gaaagaaagc agtggaaactt ggggtaaaat tgctacctgc atttcatact | 960  |
| ccctctggaa taccttgggc attgctgaat atgaaaagtg ggatcgggcg gaactggccc  | 1020 |
| tgggcctctg gaggcagcag tatcctggcc gaatttggaa ctctgcattt agagtttatg  | 1080 |
| cacttgtccc acttatcagg agaccagtc tttgccgaaa aggttatgaa aattcgaaca   | 1140 |
| gtgttgaaca aactggacaa accagaaggc ctttatccta actatctgaa cccagtagt   | 1200 |
| ggacagtggg gtcaacatca tgtgtcgggt ggaggacttg gagacagctt ttatgaatat  | 1260 |
| ttgcttaagg cgtggttaat gtctgacaag acagatctcg aagccaagaa gatgtatttt  | 1320 |
| gatgctgttc aggccatcga gactcacttg atccgcaagt caagtggggg actaacgtac  | 1380 |
| atcgagagtg ggaagggggg cctcctggaa cacaagatgg gccacctgac gtgctttgca  | 1440 |
| ggaggcatgt ttgcacttgg ggcagatgga gctccggaag cccgggcca aactacctt    | 1500 |
| gaactcggag ctgaaattgc ccgcacttgt catgaatctt ataatcgta atatgtgaag   | 1560 |
| ttgggaccgg aagcgtttcg atttgatggc ggtgtggaag ctattgccac gaggcaaat   | 1620 |
| gaaaagtatt acatcttacg gcccgaggtc atcgagacat acatgtacat gtggcgactg  | 1680 |
| actcacgacc ccaagtacag gacctgggc tgggaagccg tggaggctct agaaagtcac   | 1740 |
| tgcagagtga acggaggcta ctcaggctta cgggatgttt acattgccc tgagagttat   | 1800 |
| gacgatgtcc agcaaagttt cttcctggca gagacactga agtatttgta cttgatattt  | 1860 |
| tccgatgatg accttcttcc actagaacac tggatcttca acaccgaggc tcatcctttc  | 1920 |
| cctatactcc gtgaacagaa gaaggaaatt gatggcaaag agaaatga               | 1968 |

<210> 51  
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 <212> PRT  
 <213> Mus musculus  
 <400> 51

GFI-108 Sequence listing.ST25

Met Pro Val Gly Gly Leu Leu Pro Leu Phe Ser Ser Pro Gly Gly Gly  
1 5 10 15  
Gly Leu Gly Ser Gly Leu Gly Gly Gly Leu Gly Gly Gly Arg Lys Gly  
20 25 30  
Ser Gly Pro Ala Ala Phe Arg Leu Thr Glu Lys Phe Val Leu Leu Leu  
35 40 45  
Val Phe Ser Ala Phe Ile Thr Leu Cys Phe Gly Ala Ile Phe Phe Leu  
50 55 60  
Pro Asp Ser Ser Lys Leu Leu Ser Gly Val Leu Phe His Ser Asn Pro  
65 70 75 80  
Ala Leu Gln Pro Pro Ala Glu His Lys Pro Gly Leu Gly Ala Arg Ala  
85 90 95  
Glu Asp Ala Ala Glu Gly Arg Val Arg His Arg Glu Glu Gly Ala Pro  
100 105 110  
Gly Asp Pro Gly Ala Gly Leu Glu Asp Asn Leu Ala Arg Ile Arg Glu  
115 120 125  
Asn His Glu Arg Ala Leu Arg Glu Ala Lys Glu Thr Leu Gln Lys Leu  
130 135 140  
Pro Glu Glu Ile Gln Arg Asp Ile Leu Leu Glu Lys Glu Lys Val Ala  
145 150 155 160  
Gln Asp Gln Leu Arg Asp Lys Asp Leu Phe Arg Gly Leu Pro Lys Val  
165 170 175  
Asp Phe Leu Pro Pro Val Gly Val Glu Asn Arg Glu Pro Ala Asp Ala  
180 185 190  
Thr Ile Arg Glu Lys Arg Ala Lys Ile Lys Glu Met Met Thr His Ala  
195 200 205  
Trp Asn Asn Tyr Lys Arg Tyr Ala Trp Gly Leu Asn Glu Leu Lys Pro  
210 215 220  
Ile Ser Lys Glu Gly His Ser Ser Ser Leu Phe Gly Asn Ile Lys Gly  
225 230 235 240  
Ala Thr Ile Val Asp Ala Leu Asp Thr Leu Phe Ile Met Gly Met Lys  
245 250 255

GFI-108 Sequence listing.ST25

Thr Glu Phe Gln Glu Ala Lys Ser Trp Ile Lys Lys Tyr Leu Asp Phe  
260 265 270

Asn Val Asn Ala Glu Val Ser Val Phe Glu Val Asn Ile Arg Phe Val  
275 280 285

Gly Gly Leu Leu Ser Ala Tyr Tyr Leu Ser Gly Glu Glu Ile Phe Arg  
290 300

Lys Lys Ala Val Glu Leu Gly Val Lys Leu Leu Pro Ala Phe His Thr  
305 310 315 320

Pro Ser Gly Ile Pro Trp Ala Leu Leu Asn Met Lys Ser Gly Ile Gly  
325 330 335

Arg Asn Trp Pro Trp Ala Ser Gly Gly Ser Ser Ile Leu Ala Glu Phe  
340 345 350

Gly Thr Leu His Leu Glu Phe Met His Leu Ser His Leu Ser Gly Asp  
355 360 365

Pro Val Phe Ala Glu Lys Val Met Lys Ile Arg Thr Val Leu Asn Lys  
370 375 380

Leu Asp Lys Pro Glu Gly Leu Tyr Pro Asn Tyr Leu Asn Pro Ser Ser  
385 390 395 400

Gly Gln Trp Gly Gln His His Val Ser Val Gly Gly Leu Gly Asp Ser  
405 410 415

Phe Tyr Glu Tyr Leu Leu Lys Ala Trp Leu Met Ser Asp Lys Thr Asp  
420 425 430

Leu Glu Ala Lys Lys Met Tyr Phe Asp Ala Val Gln Ala Ile Glu Thr  
435 440 445

His Leu Ile Arg Lys Ser Ser Gly Gly Leu Thr Tyr Ile Ala Glu Trp  
450 455 460

Lys Gly Gly Leu Leu Glu His Lys Met Gly His Leu Thr Cys Phe Ala  
465 470 475 480

Gly Gly Met Phe Ala Leu Gly Ala Asp Gly Ala Pro Glu Ala Arg Ala  
485 490 495

Gln His Tyr Leu Glu Leu Gly Ala Glu Ile Ala Arg Thr Cys His Glu  
Page 46

GFI-108 Sequence listing.ST25

500

505

510

Ser Tyr Asn Arg Thr Tyr Val Lys Leu Gly Pro Glu Ala Phe Arg Phe  
515 520 525

Asp Gly Gly Val Glu Ala Ile Ala Thr Arg Gln Asn Glu Lys Tyr Tyr  
530 535 540

Ile Leu Arg Pro Glu Val Ile Glu Thr Tyr Met Tyr Met Trp Arg Leu  
545 550 555 560

Thr His Asp Pro Lys Tyr Arg Thr Trp Ala Trp Glu Ala Val Glu Ala  
565 570 575

Leu Glu Ser His Cys Arg Val Asn Gly Gly Tyr Ser Gly Leu Arg Asp  
580 585 590

Val Tyr Ile Ala Arg Glu Ser Tyr Asp Asp Val Gln Gln Ser Phe Phe  
595 600 605

Leu Ala Glu Thr Leu Lys Tyr Leu Tyr Leu Ile Phe Ser Asp Asp Asp  
610 615 620

Leu Leu Pro Leu Glu His Trp Ile Phe Asn Thr Glu Ala His Pro Phe  
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GFI-108 Sequence listing.ST25

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GFI-108 Sequence listing.ST25

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GFI-108 Sequence listing.ST25

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GFI-108 Sequence listing.ST25

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GFI-108 Sequence listing.ST25

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GFI-108 Sequence listing.ST25

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